

# DR. BRIAN NADON

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**Bioinformatics and Genetic Research Specialist with expertise in genomics, quantitative genetics, next-generation sequencing, and development of bioinformatics pipelines**

## SELECTED EXPERIENCE

**2024 – 2025**

**SENIOR BIOINFORMATICS ENGINEER, BITSCOPIC INC.**

- Contributed key algorithmic improvements to BIAS-2015, an open source ACMG standards-based variant interpreter (<https://github.com/bitscopic/BIAS-2015>)
- Submitted above research for publication in Genome Medicine (under review)
- Successfully refactored major software Praedigene into containerized microservice architecture via docker-compose, improving deployment time and platform independence
- Developed and deployed custom reporting pipeline for BCR-ABL mutations in cancer patients
- Deployed a proof-of-concept reimplement of core genetic testing pipelines for deployment in third-party HIPAA compliant platforms (e.g. DNANexus)
- Collaborated with key stakeholders across the Veterans Affairs hospital system to deliver highly accurate and reliable clinical genetic analysis pipelines for treatment of patients with cancer and hereditary diseases

**2021 – 2024**

**BIOINFORMATICS SOFTWARE ENGINEER III, THERMO FISHER SCIENTIFIC**

- Designed and deployed efficient genetic analysis pipelines for SNP-based assays and clustering algorithms for cell-free DNA monitoring
- Developed and implemented machine learning models for predicting genetic traits from ABO genotypes while adhering to industry accuracy standards
- Created novel, high-performance graph-based methods for NGS long-read RNAseq genotyping of HLA loci, improving accuracy and runtime over industry standard software
- Administered and maintained Linux-based research clusters, ensuring optimal performance of bioinformatics pipelines in high-performance computing environments
- Collaborated with cross-functional teams to incorporate AI and ML into genetic prediction models, using both decision trees and deep learning
- Took ownership of several key internal software tools, improving processes and efficiency for assay development by automating clustering and decision-making tasks for laboratory scientists

**2019-2021**

**COMPUTATIONAL BIOLOGY RESEARCH ASSOCIATE, USDA-ARS**

- Designed, engineered, and released Python-based web app for identification of candidate genes in plants, employing AI & natural language processing, SQL backend, and Dash visualization frontend (*GeneSieve*, in submission)
- Implemented pipeline for graph-based pan-genome analysis of *Salmonella enterica* genome diversity to enable downstream AI/machine learning-driven pathogenic trait characterization
- Co-Released new reference genome sequence for *Aspergillus flavus* (strain AF13 – see publications)
- Developed training materials for new scientists in the use of HPC resources and fundamentals of data science (bash, git, python) as part of carpentries workshop
- Analyzed and published backcross genetic analysis of a new near-isogenic line of *Fusarium* in collaboration with agency researchers (see publications)

# EDUCATION

**MAY 2019**

**PH.D.**, UNIVERSITY OF GEORGIA

Major in Plant Breeding, Genetics and Genomics under advisement of Dr. Scott Jackson. Dissertation: *The Evolution of Gene and Genome Duplication in Soybean*

**MAY 2013**

**B.S.**, ARIZONA STATE UNIVERSITY

Major in Cell, Genetics, and Developmental Biology. Summa Cum Laude, Dean's list 2009-2013. Honors Thesis on genetic diversity and linkage analysis in agricultural crops.

# KEY SKILLS

## Statistical Modeling & Programming:

- Proficient in R, Python, Bash, and C# programming
- Experience with quantitative genetics software (plink, tassel, etc) and stats/viz software (ggplot2, plotly)
- Strong background in machine learning applications in genomics, including LLMs and NLP

## Genomics & Biotechnology:

- Extensive experience with NGS data analysis, including ONT and PacBio technologies
- Expertise in genetic variant analysis and interpretation as well as multi-omics analysis
- Proficient with most major bioinformatics tools and pipelines (GATK, Samtools, IGV, Freebayes, vg)

## Computing & Data Management:

- Experience with high-performance computing environments (slurm) and cloud computing (AWS/Azure/Google)
- Skilled in containerization (Docker, Singularity, Podman), workflow management (e.g. SnakeMake) and Linux
- Proficient in SQL database management and large-scale data analysis

## Research & Collaboration:

- Strong background in multi-disciplinary research team environments
- Experience in translating research findings into practical applications
- Proven ability to work autonomously and collaboratively across functional teams

# SELECTED PUBLICATIONS

- Eisenhart, Nadon, Mewton, Brickey, and Bayat. *BIAS-2015: a tool for interpreting ACMG standards in variants* (2025). Under review, *Genome Medicine*.
- Fountain, J. C., Clevenger, J. P., Nadon, B., et al. (2020). *Two new Aspergillus flavus reference genomes reveal a large insertion potentially contributing to isolate stress tolerance and aflatoxin production*. *G3: Genes, Genomes, Genetics*, 10(10), 3515-3531.
- Alexandrov, N, Wang, T, Blair, L, Nadon, B, Sayer, D. (2023). *HLA-OLI: A new MHC class I pseudogene and HLA-Y are located on a 60 kb indel in the human MHC between HLA-W and HLA-J*. *HLA*, 1-8.
- SE Gold, DW Brown, FN Williams, BD Nadon, VT Vo, CE Miller. *A Fusarium verticillioides MAT1-2 Strain near Isogenic to the Sequenced FGSC7600 Strain for Producing Homozygous Multigene Mutants*. *Journal of Fungi* 10 (8), 592